



SEQUENCE LISTING

<110> DARNAY, BRYANT G.

<120> METHODS AND COMPOSITIONS USING POLYNUCLEOTIDES AND
POLYPEPTIDES OF RANK-ASSOCIATED INHIBITOR (RAIN)

<130> UTSC:761US

<140> 10/629,329

<141> 2003-07-29

<150> 60/399,205

<151> 2002-07-29

<160> 23

<170> PatentIn Ver. 2.1

<210> 1

<211> 729

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(729)

<400> 1

atg tct ggc tgt gat gct ggg gag gga gac tgt tgt tcc cgg aga tgc 48
Met Ser Gly Cys Asp Ala Gly Glu Gly Asp Cys Cys Ser Arg Arg Cys
1 5 10 15ggc gcg cag gac aag gag cat cca aga tac ctg atc cca gaa ctt tgc 96
Gly Ala Gln Asp Lys Glu His Pro Arg Tyr Leu Ile Pro Glu Leu Cys
20 25 30aaa cag ttt tac cat tta ggc tgg gtc act ggg act gga gga gga att 144
Lys Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Ile
35 40 45agc ttg aag cat ggc gat gaa atc tac att gct cct tca gga gtg caa 192
Ser Leu Lys His Gly Asp Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln
50 55 60aag gaa cga att cag cct gaa gac atg ttt gtt tgt gat ata aat gaa 240
Lys Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu
65 70 75 80

aag gac ata agt gga cct tcg cca tcg aag aag cta aaa aaa agc cag	288		
Lys Asp Ile Ser Gly Pro Ser Pro Ser Lys Lys Leu Lys Ser Gln			
85	90	95	
tgt act cct ctt ttc atg aat gct tac aca atg aga gga gca ggt gca	336		
Cys Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala			
100	105	110	
gtg att cat acc cac tct aaa gct gct gtg atg gcc aca ctt ctc ttt	384		
Val Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe			
115	120	125	
cca gga cgg gag ttt aaa att aca cat caa gag atg ata aaa gga ata	432		
Pro Gly Arg Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile			
130	135	140	
aag aaa tgt act tcc gga ggg tat tat aga tat gat gat atg tta gtg	480		
Lys Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val			
145	150	155	160
gta ccc att att gag aat aca cct gag gag aaa ggc ctc aaa gat aga	528		
Val Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Gly Leu Lys Asp Arg			
165	170	175	
atg gct cat gca atg aat gaa tac cca gac tcc tgt gca gta ctg gtc	576		
Met Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val			
180	185	190	
aga cgt cat gga gta tat gtg tgg ggg gaa aca tgg gag aag gcc aaa	624		
Arg Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys			
195	200	205	
acc atg tgt gag tgt tat gac tat tta ttt gat att gcc gta tca atg	672		
Thr Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met			
210	215	220	
aag aaa gta gga ctt gat cct tca cag ctc cca gtt gga gaa aat gga	720		
Lys Lys Val Gly Leu Asp Pro Ser Gln Leu Pro Val Gly Glu Asn Gly			
225	230	235	240
att gtg taa	729		
Ile Val			

<210> 2

<211> 242

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Gly Cys Asp Ala Gly Glu Gly Asp Cys Cys Ser Arg Arg Cys
1 5 10 15
Gly Ala Gln Asp Lys Glu His Pro Arg Tyr Leu Ile Pro Glu Leu Cys
20 25 30
Lys Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Ile
35 40 45
Ser Leu Lys His Gly Asp Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln
50 55 60
Lys Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu
65 70 75 80
Lys Asp Ile Ser Gly Pro Ser Pro Ser Lys Lys Leu Lys Lys Ser Gln
85 90 95
Cys Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala
100 105 110
Val Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe
115 120 125
Pro Gly Arg Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile
130 135 140
Lys Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val
145 150 155 160
Val Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Gly Leu Lys Asp Arg
165 170 175
Met Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val
180 185 190
Arg Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys
195 200 205
Thr Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met
210 215 220
Lys Lys Val Gly Leu Asp Pro Ser Gln Leu Pro Val Gly Glu Asn Gly
225 230 235 240
Ile Val

<210> 3

<211> 726

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(726)

<400> 3

atg tct ggc tgt caa gct caa gga gac tgt tgc tcg cgg ccg tgt ggc 48

Met Ser Gly Cys Gln Ala Gln Gly Asp Cys Cys Ser Arg Pro Cys Gly				
1	5	10	15	
gcg cag gac aag gag cac ccc cga ttc ctg atc cca gaa ctt tgc aaa	96			
Ala Gln Asp Lys Glu His Pro Arg Phe Leu Ile Pro Glu Leu Cys Lys				
20	25	30		
cag ttt tac cat ctg ggc tgg gtc acc ggc act gga ggg gga atc agc	144			
Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Ile Ser				
35	40	45		
ttg aag cat ggc aat gaa atc tac att gct ccc tca ggc gtg caa aag	192			
Leu Lys His Gly Asn Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln Lys				
50	55	60		
gaa cgc att cag cca gaa gac atg ttt gtg tgt gac att aat gag cag	240			
Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu Gln				
65	70	75	80	
gac ata agc ggg cct cca gca tct aag aag ctg aaa aaa agc cag tgc	288			
Asp Ile Ser Gly Pro Pro Ala Ser Lys Lys Leu Lys Lys Ser Gln Cys				
85	90	95		
act cct ctt ttc atg aat gct tat acc atg aga gga gct ggc gca gtg	336			
Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala Val				
100	105	110		
att cat acc cac tct aaa gct gct gtg atg gct acc ctt ctg ttt cca	384			
Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe Pro				
115	120	125		
gga cag gag ttt aaa att aca cat caa gag atg atc aaa gga ata agg	432			
Gly Gln Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile Arg				
130	135	140		
aaa tgt acc tca gga ggc tat tac aga tac gat gat atg tta gtg gta	480			
Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val Val				
145	150	155	160	
cct att att gag aac act cct gaa gag aag gat ctc aaa gaa agg atg	528			
Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Asp Leu Lys Glu Arg Met				
165	170	175		
gct cat gcc atg aac gag tac cca gac tcc tgt gcg gtt ctt gtc cgg	576			
Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val Arg				
180	185	190		
cgt cat ggg gtg tac gtg tgg gga gaa aca tgg gag aaa gca aaa acc	624			

Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys Thr			
195	200	205	
atg tgt gag tgt tat gac tac ctg ttt gac att gct gtc tcc atg aag 672			
Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met Lys			
210	215	220	
aag atg gga ctc gat cca aca cag ctc cca gtt gga gaa aat gga att 720			
Lys Met Gly Leu Asp Pro Thr Gln Leu Pro Val Gly Glu Asn Gly Ile			
225	230	235	240
gtg taa 726			
Val			
<210> 4			
<211> 241			
<212> PRT			
<213> Mus musculus			
<400> 4			
Met Ser Gly Cys Gln Ala Gln Gly Asp Cys Cys Ser Arg Pro Cys Gly			
1	5	10	15
Ala Gln Asp Lys Glu His Pro Arg Phe Leu Ile Pro Glu Leu Cys Lys			
20	25	30	
Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Ile Ser			
35	40	45	
Leu Lys His Gly Asn Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln Lys			
50	55	60	
Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu Gln			
65	70	75	80
Asp Ile Ser Gly Pro Pro Ala Ser Lys Lys Leu Lys Lys Ser Gln Cys			
85	90	95	
Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala Val			
100	105	110	
Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe Pro			
115	120	125	
Gly Gln Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile Arg			
130	135	140	
Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val Val			
145	150	155	160
Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Asp Leu Lys Glu Arg Met			
165	170	175	
Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val Arg			
180	185	190	
Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys Thr			
195	200	205	
Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met Lys			

210 215 220
Lys Met Gly Leu Asp Pro Thr Gln Leu Pro Val Gly Glu Asn Gly Ile
225 230 235 240
Val

<210> 5
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 5
Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
1 5 10 15

Lys Thr Leu Lys Asp Arg Met Ala His Ala Met Asn Glu Tyr Pro Asp
20 25 30

Ser Cys

<210> 6
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 6
Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
1 5 10 15

Lys Thr Leu Ala Asp Ala Met Ala His Thr Met Asn Glu Tyr Pro Asp
20 25 30

Ser Cys

<210> 7

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 7
ctaagaagct tggcaagcc tgaggccag 30

<210> 8
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 8
tagttttagc ggccgcgagt ctatgtcctg aac 33

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 9
ctaaaaggat ccatgtctgg ctgtgatgct ggg 33

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 10

gattttggat ctttacacaa ttccattttc tcc

33

<210> 11
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 11
ctaaaaggat ccatgtctgg ctgtcaagct caa

33

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 12
ctaagtctag actctggctg tgatgctggg

30

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13
gattttgtcg acttagacaa ttccattttc tcc

33

<210> 14
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<400> 14
Lys Leu Gly Thr Glu Leu Gly Ser
1 5

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 15
gattttggat cccacaattc cattttctcc

30

<210> 16
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 16
ggaccttcgc catccgcggc gctaaaaaaaaa agccagtgt

39

<210> 17
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 17
acaactggctt ttttttagcg ccgcggatgg cgaagggtcc

39

<210> 18

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 18
cctgaggaga aaggcctcgc agatgccatg gctcatacaa tgaat 45

<210> 19
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 19
attcattgtatgagccattc tatctttgag gcctttctcc tcagg 45

<210> 20
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 20
cacatatact ccatgagctc tgaccagtagc tgcacagga 39

<210> 21
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 21

tcctgtgcag tactggtcag agctcatgga gatatatgtg

39

<210> 22
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 22
cgtggatccc cgggatttcc ggtggtggtg gt

32

<210> 23
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 23
gcaggatccg agctcgagtc gactca

26